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FIG 1 (I)

FIG 1 (II)

FIG 1 (III)

FIG 1

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FIGURE 1 (I)

50	GCCATCCCAT	CAACAGAAGG	TTTAAGTGGA	AATCCATTTC	ATTAGAAAAG
96	ATCGGACAAA	GGGTACTCTT	AAGCATACAA	C ATG AGG GCG GTG GCG	Met Arg Ala Val Ala ₅
138	GTT TTC TTT GCT TGC GTT CTC TTC TGT ATG GTT CAC AAA GCC	Val Phe Phe Ala Cys ₁₀	Val Leu Phe Cys ₁₅	Met Val His Lys Ala	
180	GCA CTT GCG GAT GAT AAA ACG TGC AAC CCT ACA GAT TTT ATG	Ala Leu Ala Asp ₂₀	Lys Thr Cys Asn Pro ₃₀	Thr Asp Phe Met	
222	GTT ACC CAA ACC ATA ACT GGA TTG ACA ATC GGC GGT AAA CAA	Val Thr Gln Thr Ile Thr ₃₅	Gly Leu Thr Ile Gly ₄₅	Gly Lys Gln	
264	GAG TTC GAG GTC AAT TTA ATA AAC AAT TTG TAT TGT GCA CAA	Glu Phe Glu Val Asn Leu Ile ₅₀	Asn Asn Asn Leu Tyr Cys ₆₀	Ala Gln	

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FIGURE 1 (II)

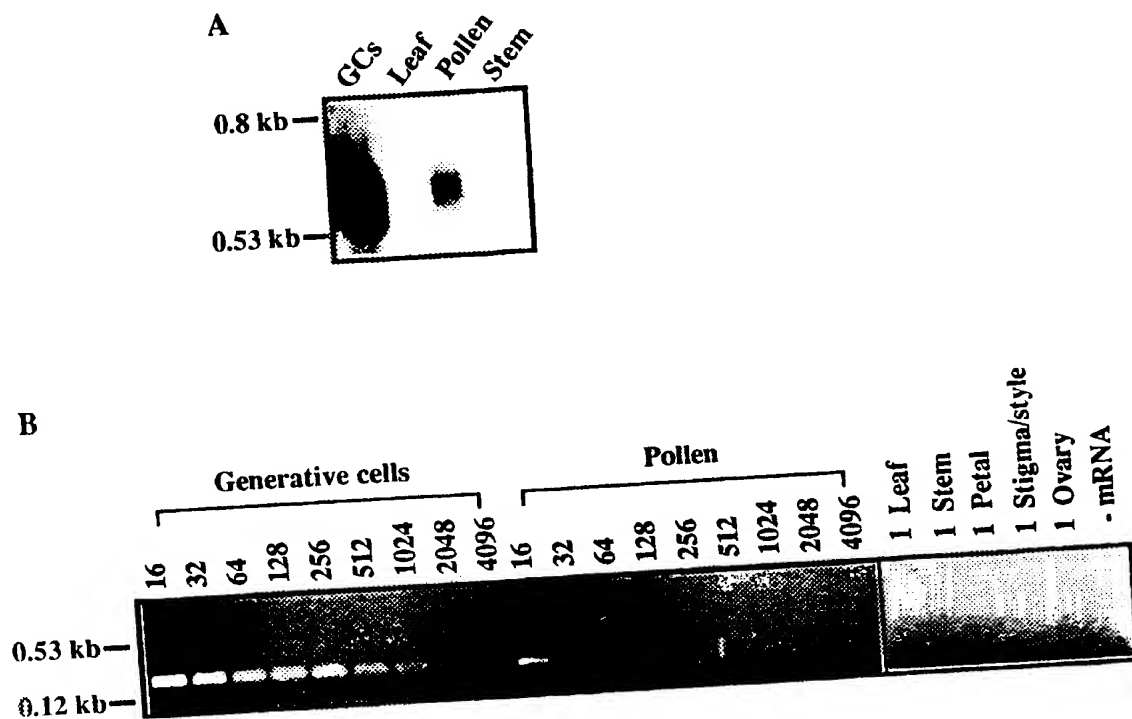
306	TCT AAT GTC AAA GTT TCA TGT GAC GGG CTT CAT ACC ACC GAA	75
	Ser Asn Val Lys Val Ser Cys Asp Gly Leu His Thr Glu	
348	CCA ATA GAT CCT CAC ATT ATC AGA CCA CTT AGT GAC GGA ACG	
	Pro Ile Asp Pro His Ile Ile Arg Pro Leu Ser Asp Gly Thr	
390	AAC AAC TGC CTT GTC AAC AAT GGA GCG CCT ATT TCT CAT GCT	
	Asn Asn Cys Leu Val Asn Asn Gly Ala Pro Ile Ser His Ala	
432	ACT CTT GTA GCA TTC AAG TAT GCC TGG GAT GTT CCT CCA TCT	
	Thr Leu Val Ala Phe Lys Tyr Ala Trp Asp Val Pro Pro Ser	
468	TTC AGC ATC ATC AGC TCT GAT ATA AAT TGC TCC TAA	
	Phe Ser Ile Ile Ser Ser Asp Ile Asn Cys Ser OCH	
515	GGAGAAA ATTCTAGTTG GCAGAGAATA ATCATATAGT CTTTTTACT	

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FIGURE 1 (III)

565	GAGCTATTTA	ATTTTTC	CAAA	TTTTCACCAA	TAAGATTATT	TTAATGGAAT
615	GTAAATGTAT	TAGAATTGAA	AAATAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA
625	AAAAAAAAAA					

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FIG 2

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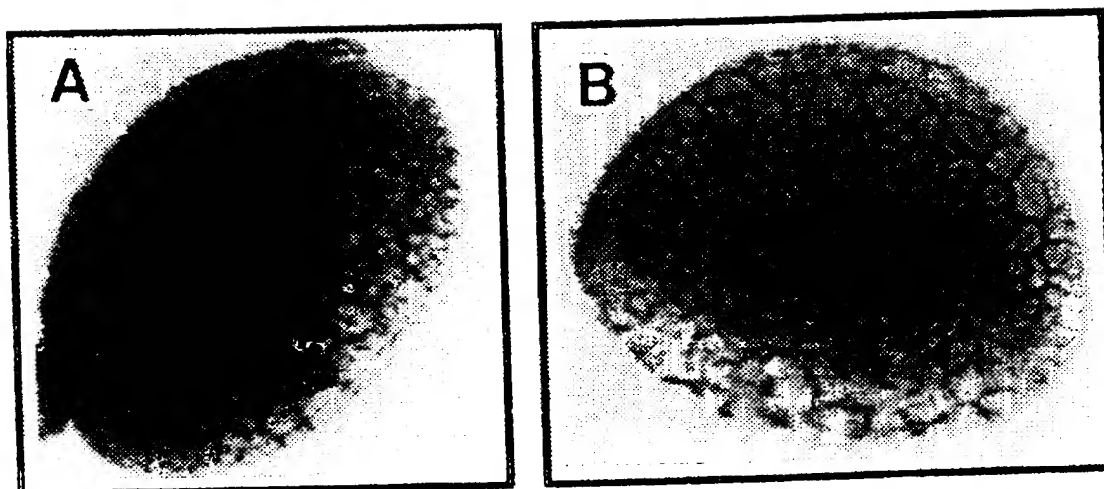


FIG 3

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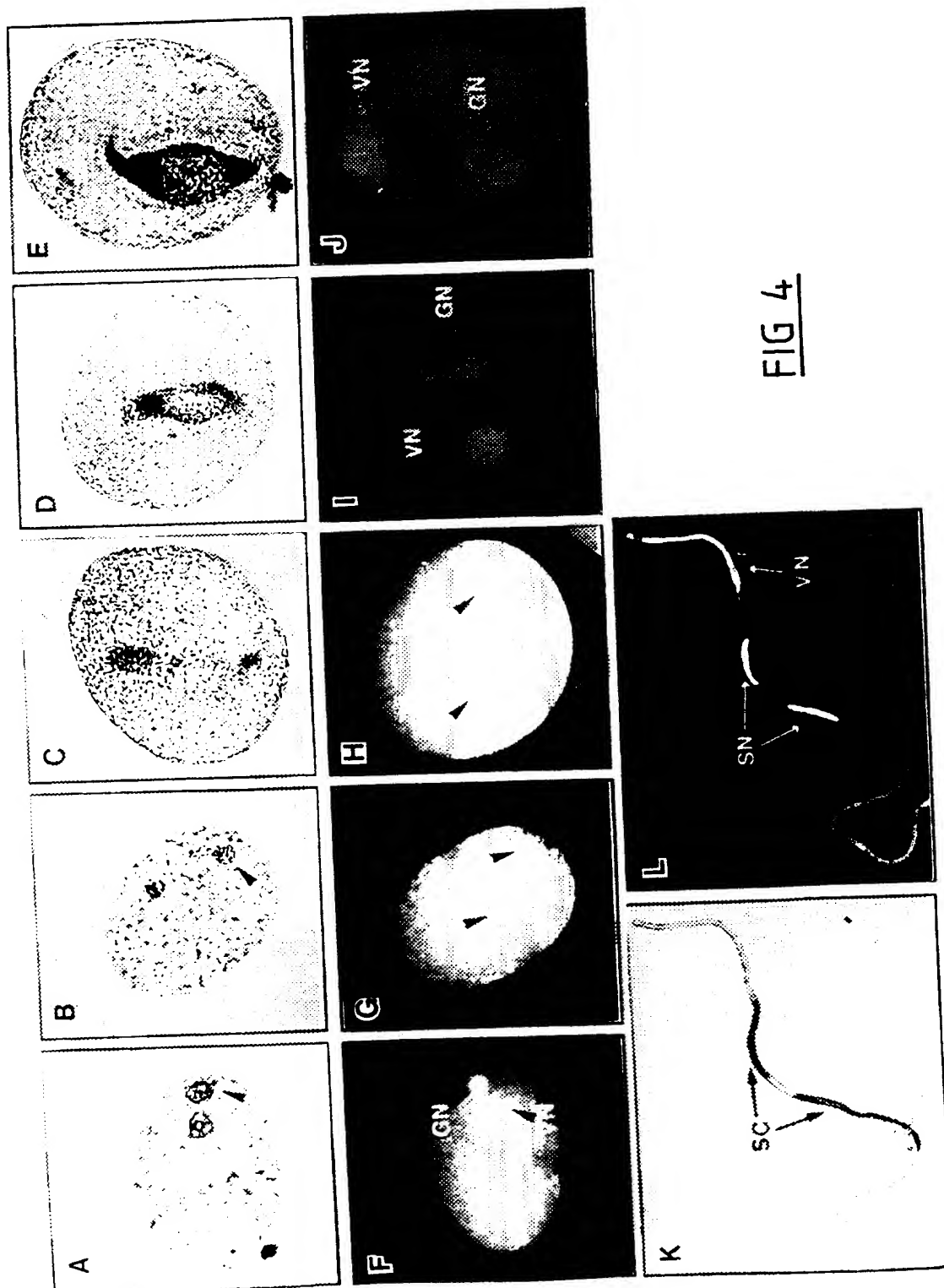


FIG 4

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FIG 5 (I)

FIG 5 (II)

FIG 5 (III)

FIG 5

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FIGURE 5 (I)

48	GAAAGTTGAA	ACATCTCCAT	CAAACTCTAG	AGTCAGATTT	CCCACAAG
87	ATG ATT TCA TCG GCA AAT AAC AAA GGC GCC GGC ACA AGC				
	Met Ile Ser Ser Ala Asn Asn Lys Gly Ala Gly Thr Ser				
		5	10		
126	CGC CGC AAG CTC CGT TCT GAG AAG GCT GCA CTC CAG TTC				
	Arg Arg Lys Leu Arg Ser Glu Lys Ala Ala Leu Gln Phe				
		15	20	25	
165	TCC GTC AGT CGC GTC GAA TAC TCC CTC AAG AAG GGC CGC				
	Ser Val Ser Arg Val Glu Tyr Ser Leu Lys Lys Gly Arg				
		30	35		
204	TAT TGC AGG CGC TTA GGC GCT ACG GCC CCC GTC TAC CTA				
	Tyr Cys Arg Arg Leu Gly Ala Thr Ala Pro Val Tyr Leu				
		40	45	50	
243	GCC GCC GTC CTT GAA AAC CTC GTG GCC GAA GTG TTG GAC				
	Ala Ala Val Leu Glu Asn Leu Val Ala Glu Val Leu Asp				
		55	60	65	

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FIGURE 5 (II)

ATG GCG GCG AAC GTG ACA GAA GAA ACA TCC CCC ATT GTT	282
Met Ala Ala Asn Val Thr Glu Glu Thr Ser Pro Ile Val	
	70
	75
ATC AAA CCG AGG CAT ATT ATG CTT GCC CCC AGG AAT GAT	321
Ile Lys Pro Arg His Ile Met Leu Ala Pro Arg Asn Asp	
	80
	85
GTA GAA GTT GAA CAA GCT GTT TCA CGG TGT CAC CAT CTC	360
Val Glu Val Glu Gln Ala Val Ser Arg Cys His His Leu	
	95
	100
GGC ATC AGG TGT CGT CCC TAAACACACGC AAAGAGCTGG	398
Gly Ile Arg Cys Arg Pro	
	110
ACCGTCGCAA ACGCCGTTCC ACCTTTCAGC CGGATTAGTT CTTGATATTT	448
CATTCTATCA ATCTTGTTA TGTGACTGTG ATTTTCGTT TTGTGTTGAA	498

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FIGURE 5 (III)

548

CTAAGCCCCC TAATCTGGAT TTCTCGTTT ATGTTGAACT AAGTCTGTGC

587

ACTCTTGAAG TAAAAAAA AAAAAAAA AAAAAAAA

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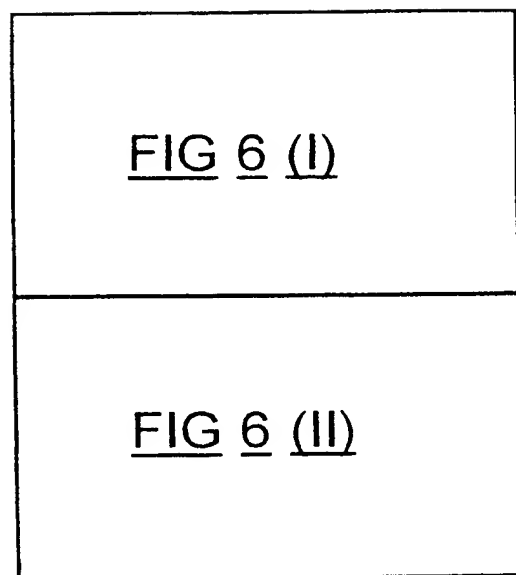


FIG 6

FIGURE 6 (I)

[illegible]

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FIGURE 6 (II)

237	GCG AGA TTT CAC AGG AAA CTG CCA TTC CAA GGG CTG GTG Ala Arg Phe His 65	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70
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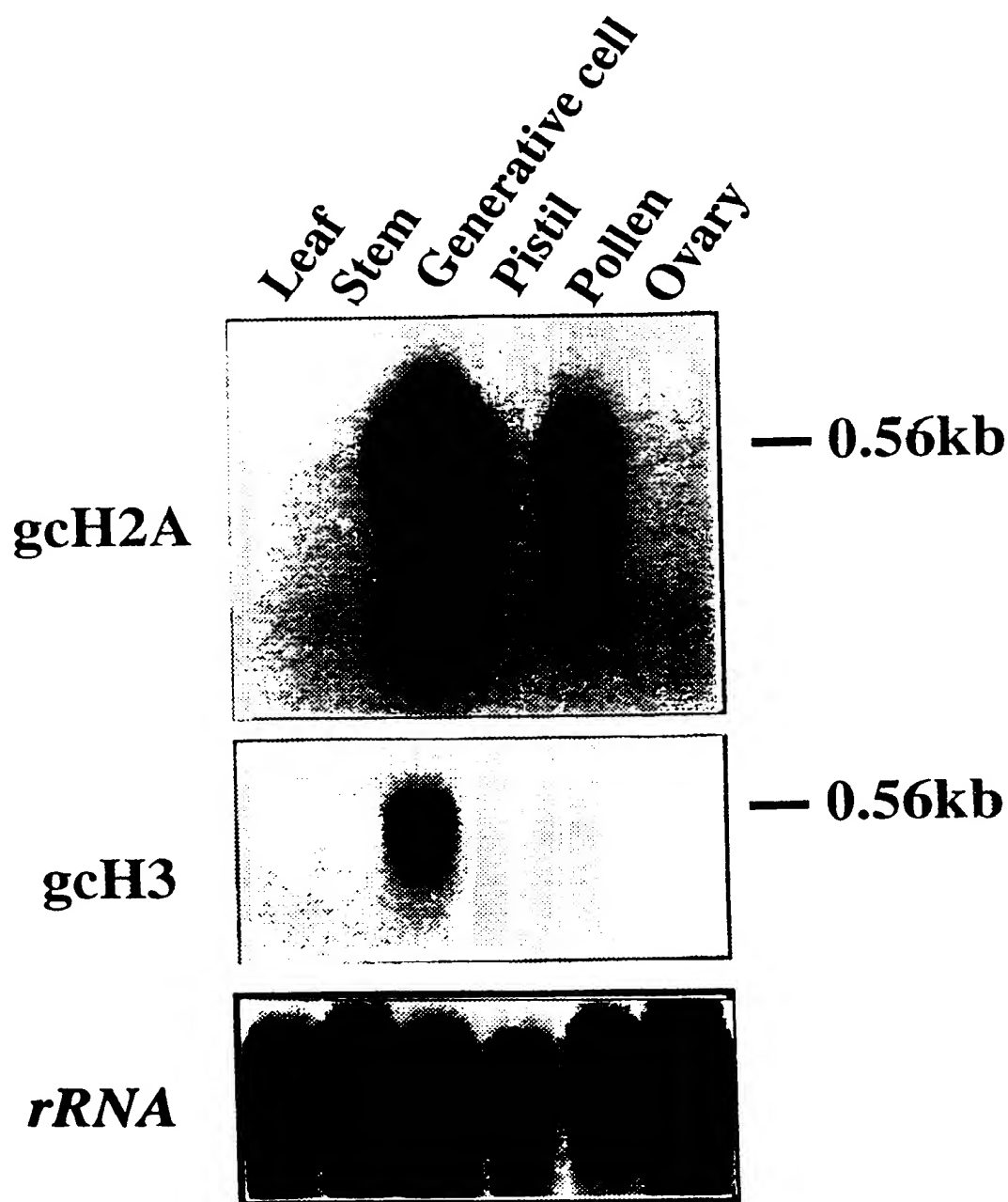


FIG 7

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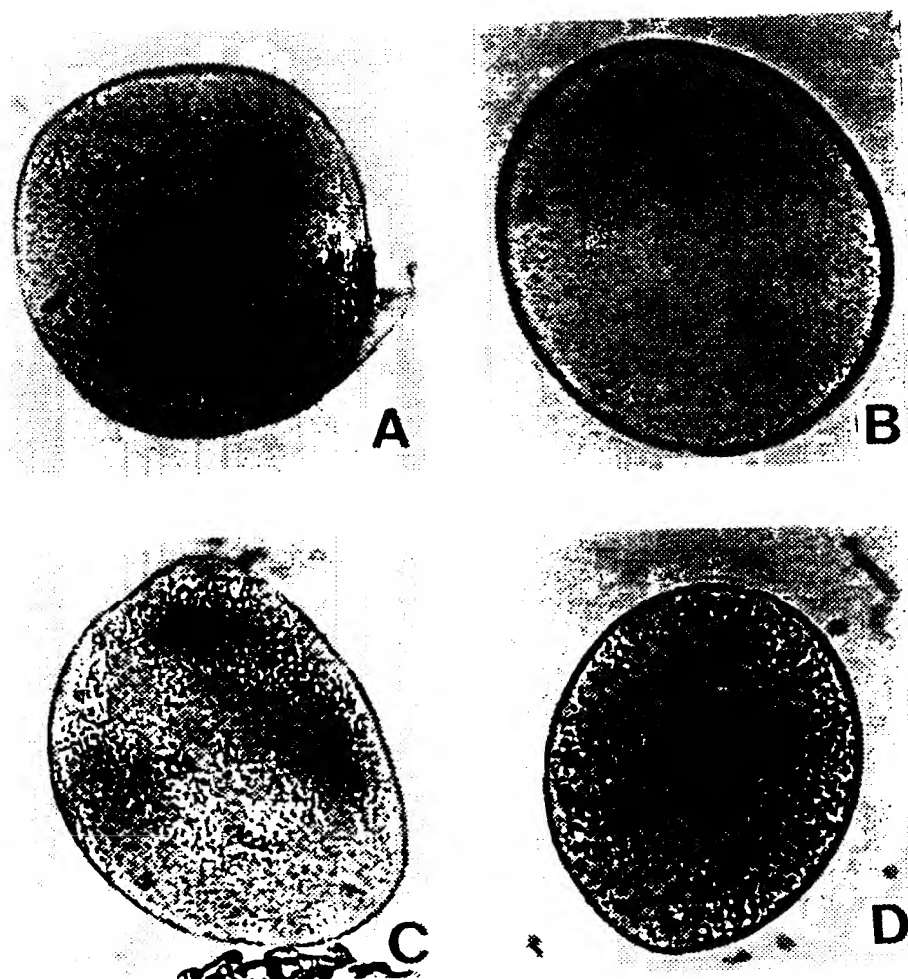


FIG 8

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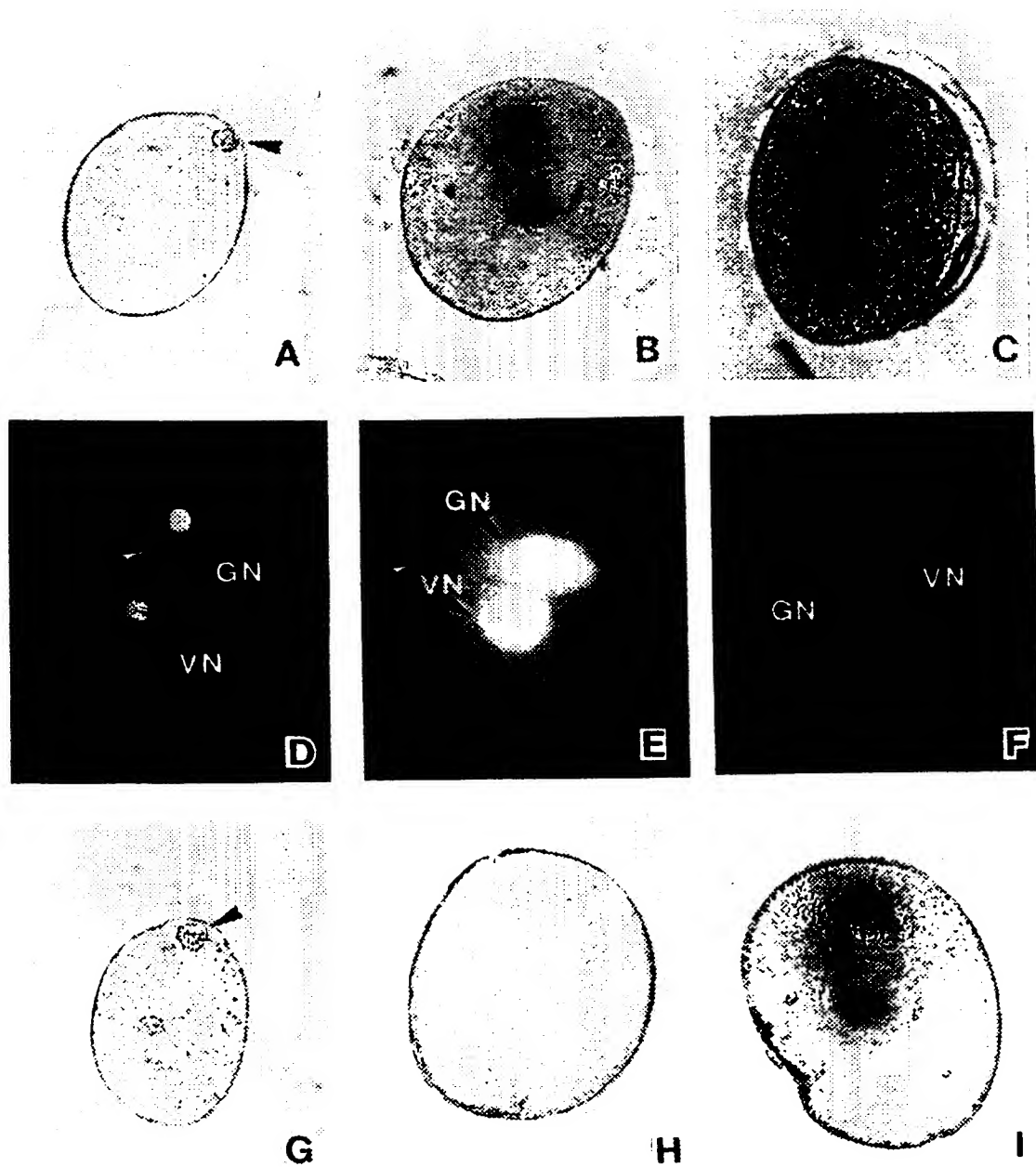


FIG 9

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FIG 10 (I)

FIG 10 (II)

FIG 10

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FIGURE 10 (I)

50	GGAGGGTGTT	GGAATTAGGT	TTGCCCTAGG	TTTAGAGAAA
100	TAGTCAAAAT	TGTCCTATTC	TATAGGCATG	GAGTTAATTA
150	TCCTATAATT	TCTCTTCTTG	TATGCTCAA	TTTAATGAAT
200	AGATAATTAA	GTTTGTAGC	AATTCTTCC	TATCAACAAT
250	TGTTAGATTG	CTTTGGTGAT	TATATTGAT	GTAAGAATGT
300	GTAGTGAAA	GATTGTGATT	ATTCATTTCG	AATTGTTAGA
350	GCCCCATCGC	TAAATGCCCTTA	TAGTACTCGA	GAATAGAAGA
400	TGAAAAATCC	CATTCTTTGT	AGTAGGAGTA	TTTTTCATTAT
450	TCCATTGAAT	GTTAACCACCT	TGCCATTTCAT	TGGCAGAGTT
500	CCGACCATCT	AGTGATCCGT	GGGATATTGA	TCAATGAAAT
550	TGTGAGAACG	GGCTTCTGGG	AGAGAAAAGC	CTGATATGAA
600	CACGTAGGCT	GATTATGTTA	ACGGATGGAG	GGCTGAATTT
650	GGGTGCTGTA	GAGACAGAAT	TTGAAAGTTC	CCCTAATTCT
700	GAACCTGGGC	GGGGCTGGGA	TTTTTACTCTT	AACGTGAAGA
750	GAATTGACAG	CTTGGAAGTC	GATCCAGTAT	TTGCAGCAGT

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FIGURE 10 (II)

TGGTTGGACA	GTTACATCGG	TCAGAGAAATG	CGTCTATATA	ATTCCCCCAA	800
TGCGGCAGTG	AAAATC CC AT	CCCATCAACA	GAAAGTTTAA	GTGGAAACCC	850
ATTCCAATAG	AGAAGATCGA	ACAAAGGGTA	TTTAAACATA	CAA ATG GGGG	900
CAGTGGTGTT	TCTTTTGCT	TGCGTCTCT	TCTGTATGGT	TCACA	945

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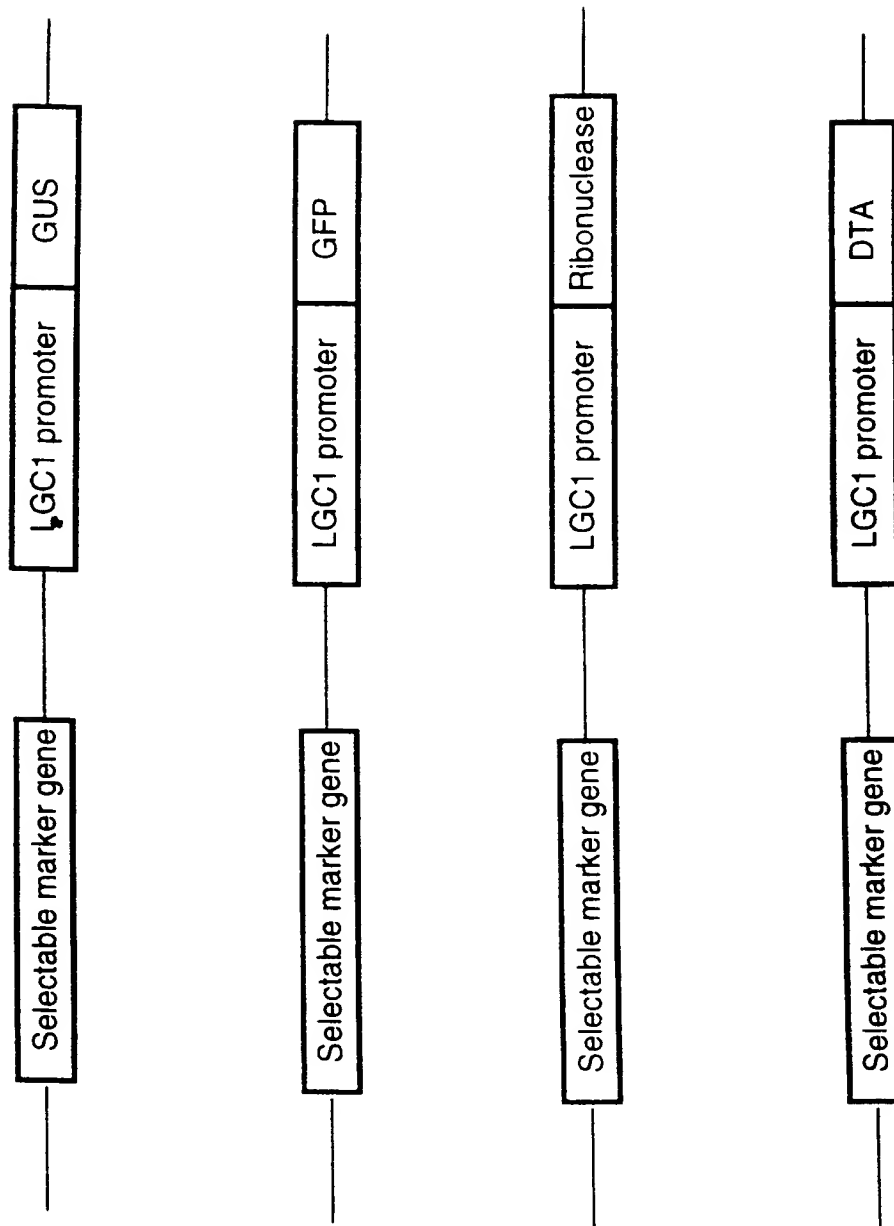
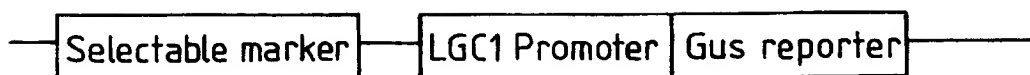


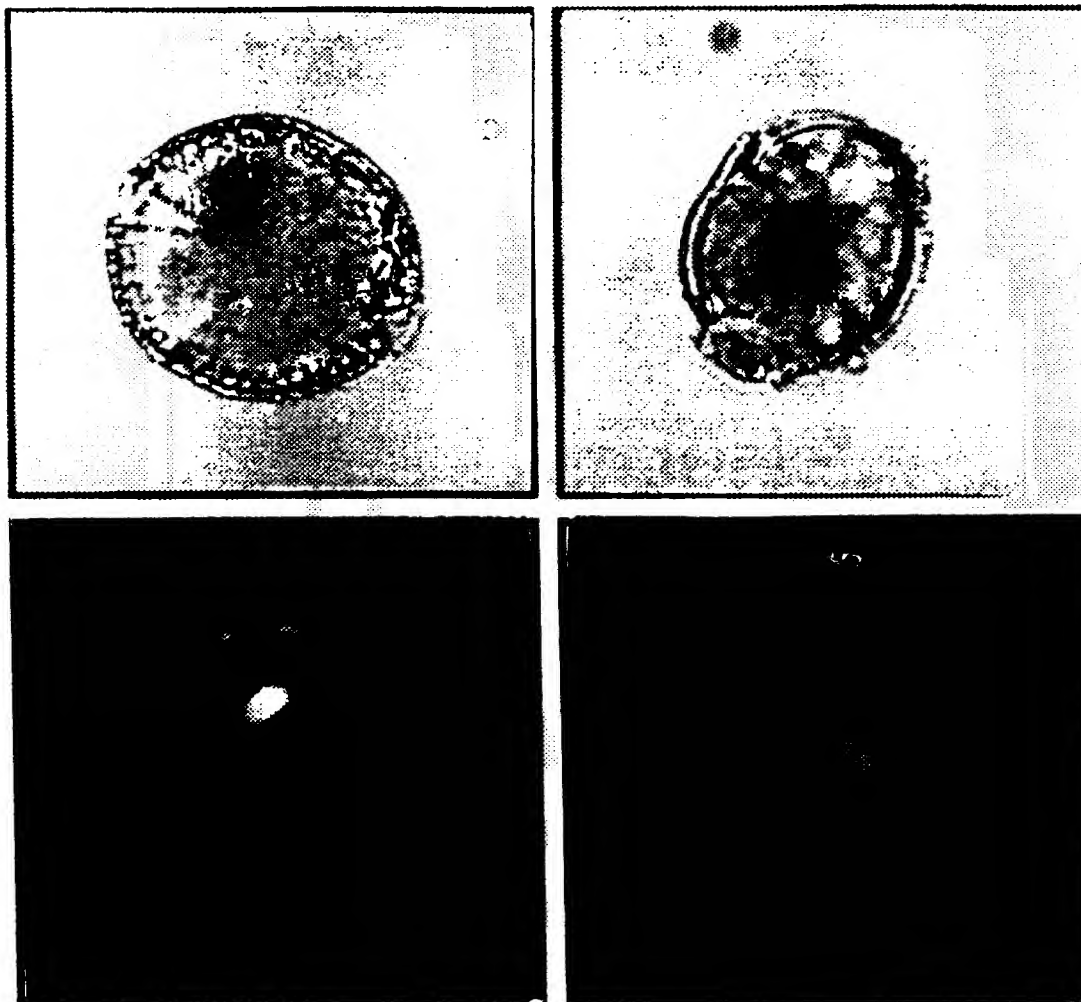
FIG 11

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A



B

FIG 12